



0.02

**Figure S4.** Phylogenetic tree based on 16S rRNA gene sequences of *Mollicutes*. The tree was generated using neighbor-joining algorithm, with kimura-2 parameter and 1,000 bootstrap replications (MEGA 5 software). *Bacillus subtilis* subsp. *subtilis* str. 168 was used as outgroup. Bar shows substitution per nucleotide.